

SEQUENCE LISTING

<110> Walke, D. Wade
Donoho, Gregory
Scoville, John
Hilbun, Erin,
Zambrowicz, Brian
Turner, C. Alexander Jr.

<120> Novel Human Proteins and Polynucleotides Encoding the Same

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<150> US 60/192,218

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Phe	Glu	Pro	Asn	Phe	Cys	Gln	Asp	Asn	Pro	Arg	Ser	Pro	Thr	Ser	Ser	115	120	125
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Cys	Ile	Val	Val	Gly	Ile	Pro	Pro	Pro	Gln	Val	Arg	Trp	Tyr	Cys	Glu
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 Arg Lys Arg Leu Ser Pro Asp Gln Met Lys His Ser Pro Asn Leu Ser
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 Phe Glu Pro Asn Phe Cys Gln Asp Asn Pro Arg Ser Pro Thr Ser Ser
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Ala Phe Leu Ser Gln Glu Glu Leu Asp Glu Ser Val Asn Leu Ala Arg
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	260	265
Gln Lys Leu Arg Ser Arg Glu Val Pro Glu Gly Thr Arg Val Gln Leu		270
	275	280
Asp Cys Ile Val Val Gly Ile Pro Pro Pro Gln Val Arg Trp Tyr Cys		285
	290	295
Glu Gly Lys Glu Leu Glu Asn Ser Pro Asp Ile His Ile Val Gln Ala		300
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Gly Asn Leu His Ser Leu Thr Ile Ala Glu Ala Phe Glu Glu Asp Thr		320
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Ser	Ala	Glu	Ile	Tyr	Ile	Glu	Gly	Val	Ser	Ser	Ser	Asp	Ser	Glu	Gly
	355						360					365			
Asp	Pro	Asn	Lys	Glu	Glu	Met	Asn	Arg	Ile	Gln	Lys	Pro	Asn	Glu	Val
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Phe Thr Cys	Thr Ala Ser Asn Lys Tyr Gly Thr Val Ser Ser Ile Ala				
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Gln Leu His	Val Arg Gly Asn Glu Asp Leu Ser Asn Asn Gly Ser Leu				
	530		535		540
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agacagacca	ggccccgattc	tttscaggag	aggttcaacg	gacaggcaac	aaaaacccca	1920
gagccttctt	tccccgtgaa	agagccccct	ccagttcttg	ccaaacccaa	acttgattcc	1980
actcagttac	aacagcttca	taaccaagtc	ttactggaac	aacaccaatt	gcaaaaccca	2040
cctccttcat	ctcctaagga	gtttcctttc	arcatgactg	ttttgaactc	caatgctccc	2100
ccagcgggtga	caacatccar	taagcagggtg	aaggctcctt	catcacagac	gttcagcttg	2160
gcccggccga	agtatttctt	ccctccacg	aacaccaccg	cagcaactgt	ggcccccttc	2220
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<210> 14
 <211> 754
 <212> PRT
 <213> homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(754)
 <223> Xaa = Any Amino Acid

<400> 14
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 Arg Glu Ser Tyr Leu Ala Glu Thr Arg His Arg Gly Asn Asn Glu Arg
 20 25 30
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 35 40 45
 Gly Ala Ala Glu Gly Gly Gly Gln Asp Asp Leu Pro Asp Leu Ser
 50 55 60
 Ala Phe Leu Ser Gln Glu Leu Asp Glu Ser Val Asn Leu Ala Arg
 65 70 75 80
 Leu Ala Ile Asn Tyr Asp Pro Leu Glu Lys Ala Asp Glu Thr Gln Ala
 85 90 95
 Arg Lys Arg Leu Ser Pro Asp Gln Met Lys His Ser Pro Asn Leu Ser
 100 105 110
 Phe Glu Pro Asn Phe Cys Gln Asp Asn Pro Arg Ser Pro Thr Ser Ser
 115 120 125
 Lys Glu Ser Pro Gln Glu Ala Lys Arg Pro Gln Tyr Cys Ser Glu Thr
 130 135 140
 Gln Ser Lys Lys Val Phe Leu Asn Lys Ala Ala Asp Phe Ile Glu Glu
 145 150 155 160
 Leu Ser Ser Leu Phe Lys Ser His Ser Ser Lys Arg Ile Arg Pro Arg
 165 170 175
 Ala Cys Lys Asn His Lys Ser Lys Leu Glu Ser Gln Asn Lys Val Met
 180 185 190
 Gln Glu Asn Ser Ser Ser Phe Ser Asp Leu Ser Glu Arg Arg Glu Arg
 195 200 205
 Ser Ser Val Pro Ile Pro Ile Pro Ala Asp Thr Arg Asp Asn Glu Val
 210 215 220
 Asn His Ala Leu Glu Gln Gln Glu Ala Lys Arg Arg Glu Ala Glu Gln
 225 230 235 240
 Ala Ala Ser Glu Ala Ala Gly Gly Asp Thr Thr Pro Gly Ser Ser Pro
 245 250 255
 Ser Ser Leu Tyr Tyr Glu Glu Pro Leu Gly Gln Pro Pro Arg Phe Thr
 260 265 270
 Gln Lys Leu Arg Ser Arg Glu Val Pro Glu Gly Thr Arg Val Gln Leu
 275 280 285
 Asp Cys Ile Val Val Gly Ile Pro Pro Pro Gln Val Arg Trp Tyr Cys
 290 295 300
 Glu Gly Lys Glu Leu Glu Asn Ser Pro Asp Ile His Ile Val Gln Ala
 305 310 315 320
 Gly Asn Leu His Ser Leu Thr Ile Ala Glu Ala Phe Glu Glu Asp Thr
 325 330 335
 Gly Arg Tyr Ser Cys Phe Ala Ser Asn Ile Tyr Gly Thr Asp Ser Thr
 340 345 350
 Ser Ala Glu Ile Tyr Ile Glu Gly Val Ser Ser Ser Asp Ser Glu Gly

	355		360		365										
Asp	Pro	Asn	Lys	Glu	Glu	Met	Asn	Arg	Ile	Gln	Lys	Pro	Asn	Glu	Val
	370					375					380				
Ser	Ser	Pro	Pro	Thr	Thr	Ser	Ala	Val	Ile	Pro	Pro	Ala	Val	Pro	Gln
385						390					395				400
Ala	Gln	His	Leu	Val	Ala	Gln	Pro	Arg	Val	Ala	Thr	Ile	Gln	Gln	Cys
			405						410					415	
Gln	Ser	Pro	Thr	Asn	Tyr	Leu	Gln	Gly	Leu	Asp	Gly	Lys	Pro	Ile	Ile
			420					425					430		
Ala	Ala	Pro	Val	Phe	Thr	Lys	Met	Leu	Gln	Asn	Leu	Ser	Ala	Ser	Glu
		435					440					445			
Gly	Gln	Leu	Val	Val	Phe	Glu	Cys	Arg	Val	Lys	Gly	Ala	Pro	Ser	Pro
	450					455					460				
Lys	Val	Glu	Trp	Tyr	Arg	Glu	Gly	Thr	Leu	Ile	Glu	Asp	Ser	Pro	Asp
465					470					475					480
Phe	Arg	Ile	Leu	Gln	Lys	Lys	Pro	Arg	Ser	Met	Ala	Glu	Pro	Glu	Glu
			485						490					495	
Ile	Cys	Thr	Leu	Val	Ile	Ala	Glu	Val	Phe	Ala	Glu	Asp	Ser	Gly	Cys
		500						505					510		
Phe	Thr	Cys	Thr	Ala	Ser	Asn	Lys	Tyr	Gly	Thr	Val	Ser	Ser	Ile	Ala
	515						520					525			
Gln	Leu	His	Val	Arg	Gly	Asn	Glu	Asp	Leu	Ser	Asn	Asn	Gly	Ser	Leu
	530					535					540				
His	Ser	Ala	Asn	Ser	Thr	Asn	Leu	Ala	Ala	Ile	Glu	Pro	Gln	Pro	
545					550					555					560
Ser	Pro	Pro	His	Ser	Glu	Pro	Pro	Ser	Val	Glu	Gln	Pro	Pro	Lys	Pro
			565						570					575	
Lys	Leu	Glu	Gly	Val	Leu	Val	Asn	His	Asn	Glu	Pro	Arg	Ser	Ser	Ser
			580					585					590		
Arg	Ile	Gly	Leu	Arg	Val	His	Phe	Asn	Leu	Pro	Glu	Asp	Asp	Lys	Gly
		595					600					605			
Ser	Glu	Ala	Ser	Ser	Glu	Ala	Gly	Val	Val	Thr	Thr	Arg	Gln	Thr	Arg
	610					615					620				
Pro	Asp	Ser	Xaa	Gln	Glu	Arg	Phe	Asn	Gly	Gln	Ala	Thr	Lys	Thr	Pro
625					630					635					640
Glu	Pro	Ser	Phe	Pro	Val	Lys	Glu	Pro	Pro	Pro	Val	Leu	Ala	Lys	Pro
			645						650					655	
Lys	Leu	Asp	Ser	Thr	Gln	Leu	Gln	Gln	Leu	His	Asn	Gln	Val	Leu	Leu
		660					665					670			
Glu	Gln	His	Gln	Leu	Gln	Asn	Pro	Pro	Pro	Ser	Ser	Pro	Lys	Glu	Phe
		675					680					685			
Pro	Phe	Xaa	Met	Thr	Val	Leu	Asn	Ser	Asn	Ala	Pro	Pro	Ala	Val	Thr
	690					695				700					
Thr	Ser	Xaa	Lys	Gln	Val	Lys	Ala	Pro	Ser	Ser	Gln	Thr	Phe	Ser	Leu
705					710					715					720
Ala	Arg	Pro	Lys	Tyr	Phe	Phe	Pro	Ser	Thr	Asn	Thr	Thr	Ala	Ala	Thr
			725						730				735		
Val	Ala	Pro	Ser	Ser	Ser	Pro	Val	Phe	Thr	Leu	Ser	Ser	Ile	Pro	Pro
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Gln	Thr														

<210> 15

<211> 3138

<212> DNA

<213> homo sapiens

<400> 15

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aatcgaatcc	agaagccaaa	tgagggtgca	tctcctccca	ctacctctgc	agtcattcct	360
ccagcagtac	cccaagccca	gcatttgggtg	gcccacacctc	gtgtggcaac	catccagcag	420
tgctcagagcc	ccaccaatta	cttgccaggga	ttggatggaa	aacctatcat	tgccagctcct	480
gtgttttacia	agatgctaca	aaatttgtca	gcttctgagg	gtccagctggt	tgtctttgaa	540
tgccagagtaa	aaggagctcc	atctcctaag	gttgagtgggt	atagagaagg	gactttaata	600
gaagattctc	cagattttag	gattttacag	aaaaaacctc	gatccatggc	agagccagag	660
gagatttgca	ccttgggtcat	tgctgagggtg	tttgccagaag	attctgggtg	cttcacatgt	720
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caattgcaaa	accacactcc	ttcatctcct	aaggagtttc	ctttccarcat	gactgttttg	1260
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<210> 16

<211> 1045
 <212> PRT
 <213> homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(1045)
 <223> Xaa = Any Amino Acid

<400> 16

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		20						25					30		
Glu	Leu	Glu	Asn	Ser	Pro	Asp	Ile	His	Ile	Val	Gln	Ala	Gly	Asn	Leu
		35					40					45			
His	Ser	Leu	Thr	Ile	Ala	Glu	Ala	Phe	Glu	Glu	Asp	Thr	Gly	Arg	Tyr
	50					55					60				
Ser	Cys	Phe	Ala	Ser	Asn	Ile	Tyr	Gly	Thr	Asp	Ser	Thr	Ser	Ala	Glu
65					70					75					80
Ile	Tyr	Ile	Glu	Gly	Val	Ser	Ser	Ser	Asp	Ser	Glu	Gly	Asp	Pro	Asn
			85						90					95	
Lys	Glu	Glu	Met	Asn	Arg	Ile	Gln	Lys	Pro	Asn	Glu	Val	Ser	Ser	Pro
			100					105					110		
Pro	Thr	Thr	Ser	Ala	Val	Ile	Pro	Pro	Ala	Val	Pro	Gln	Ala	Gln	His
		115					120					125			
Leu	Val	Ala	Gln	Pro	Arg	Val	Ala	Thr	Ile	Gln	Gln	Cys	Gln	Ser	Pro
		130				135					140				
Thr	Asn	Tyr	Leu	Gln	Gly	Leu	Asp	Gly	Lys	Pro	Ile	Ile	Ala	Ala	Pro
145				150						155					160
Val	Phe	Thr	Lys	Met	Leu	Gln	Asn	Leu	Ser	Ala	Ser	Glu	Gly	Gln	Leu
			165						170					175	
Val	Val	Phe	Glu	Cys	Arg	Val	Lys	Gly	Ala	Pro	Ser	Pro	Lys	Val	Glu
		180						185					190		
Trp	Tyr	Arg	Glu	Gly	Thr	Leu	Ile	Glu	Asp	Ser	Pro	Asp	Phe	Arg	Ile
		195				200						205			
Leu	Gln	Lys	Lys	Pro	Arg	Ser	Met	Ala	Glu	Pro	Glu	Glu	Ile	Cys	Thr
	210				215						220				
Leu	Val	Ile	Ala	Glu	Val	Phe	Ala	Glu	Asp	Ser	Gly	Cys	Phe	Thr	Cys
225			230						235					240	
Thr	Ala	Ser	Asn	Lys	Tyr	Gly	Thr	Val	Ser	Ser	Ile	Ala	Gln	Leu	His
			245					250					255		
Val	Arg	Gly	Asn	Glu	Asp	Leu	Ser	Asn	Asn	Gly	Ser	Leu	His	Ser	Ala
		260						265					270		
Asn	Ser	Thr	Thr	Asn	Leu	Ala	Ala	Ile	Glu	Pro	Gln	Pro	Ser	Pro	Pro
	275					280						285			
His	Ser	Glu	Pro	Pro	Ser	Val	Glu	Gln	Pro	Pro	Lys	Pro	Lys	Leu	Glu
	290				295						300				
Gly	Val	Leu	Val	Asn	His	Asn	Glu	Pro	Arg	Ser	Ser	Ser	Arg	Ile	Gly
305				310					315					320	
Leu	Arg	Val	His	Phe	Asn	Leu	Pro	Glu	Asp	Asp	Lys	Gly	Ser	Glu	Ala
			325					330					335		
Ser	Ser	Glu	Ala	Gly	Val	Val	Thr	Thr	Arg	Gln	Thr	Arg	Pro	Asp	Ser
		340					345					350			
Xaa	Gln	Glu	Arg	Phe	Asn	Gly	Gln	Ala	Thr	Lys	Thr	Pro	Glu	Pro	Ser
	355					360						365			

Leu Asp Cys Lys Val Ser Gly Leu Pro Pro Pro Glu Leu Thr Trp Leu
 820 825 830
 Leu Asn Gly Gln Pro Val Leu Pro Asp Ala Ser His Lys Met Leu Val
 835 840 845
 Arg Glu Thr Gly Val His Ser Leu Leu Ile Asp Pro Leu Thr Gln Arg
 850 855 860
 Asp Ala Gly Thr Tyr Lys Cys Ile Ala Thr Asn Lys Thr Gly Gln Asn
 865 870 875 880
 Ser Phe Ser Leu Glu Leu Ser Val Val Ala Lys Glu Val Lys Lys Ala
 885 890 895
 Pro Val Ile Leu Glu Lys Leu Gln Asn Cys Gly Val Pro Glu Gly His
 900 905 910
 Pro Val Arg Leu Glu Cys Arg Val Ile Gly Met Pro Pro Pro Val Phe
 915 920 925
 Tyr Trp Lys Lys Asp Asn Glu Thr Ile Pro Cys Thr Arg Glu Arg Ile
 930 935 940
 Ser Met His Gln Asp Thr Thr Gly Tyr Ala Cys Leu Leu Ile Gln Pro
 945 950 955 960
 Ala Lys Lys Ser Asp Ala Gly Trp Tyr Thr Leu Ser Ala Lys Asn Glu
 965 970 975
 Ala Gly Ile Val Ser Cys Thr Ala Arg Leu Asp Ile Tyr Ala Gln Trp
 980 985 990
 His His Gln Ile Pro Pro Pro Met Ser Val Arg Pro Ser Gly Ser Arg
 995 1000 1005
 Tyr Gly Ser Leu Thr Ser Lys Gly Leu Asp Ile Phe Ser Ala Phe Ser
 1010 1015 1020
 Ser Met Glu Ser Thr Met Val Tyr Ser Cys Ser Ser Arg Ser Val Val
 1025 1030 1035 1040
 Glu Ser Asp Glu Leu
 1045

<210> 17
 <211> 309
 <212> DNA
 <213> homo sapiens

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 cacatcgtcc aggcaggaaa tctgcactca ctgaccattg cggaagcctt tgaagaggac 180
 acaggacgct attcctgctt tgcttctaac atctatggga cagattcgac ttctgctgag 240
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<210> 18
 <211> 102
 <212> PRT
 <213> homo sapiens

<400> 18
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 Ser Leu Ala Phe Leu Trp Ile Ile Pro Met Trp Tyr Cys Glu Gly Lys
 20 25 30
 Glu Leu Glu Asn Ser Pro Asp Ile His Ile Val Gln Ala Gly Asn Leu
 35 40 45

His Ser Leu Thr Ile Ala Glu Ala Phe Glu Glu Asp Thr Gly Arg Tyr
50 55 60
Ser Cys Phe Ala Ser Asn Ile Tyr Gly Thr Asp Ser Thr Ser Ala Glu
65 70 75 80
Ile Tyr Ile Glu Gly Val Ser Ser Ser Asp Ser Glu Gly Asp Pro Asn
85 90 95
Lys Glu Glu Met Asn Arg
100

<210> 19
<211> 435
<212> DNA
<213> homo sapiens

<400> 19
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cacatcgctc aggcaggaaa tctgcactca ctgaccattg cggaagcctt tgaagaggac 180
acaggacgct attcctgctt tgcttctaac atctatggga cagattcgac ttctgctgag 240
atztatatag aaggggtttc ttcttctgac tcagaaggcg accctaacaa ggaagagatg 300
aatcgtgtca gagccccacc aattacttgc agggattgga tggaaaacct atcattgcag 360
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ttgaatgcag agtaa 435

<210> 20
<211> 144
<212> PRT
<213> homo sapiens

<400> 20
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20 25 30
Glu Leu Glu Asn Ser Pro Asp Ile His Ile Val Gln Ala Gly Asn Leu
35 40 45
His Ser Leu Thr Ile Ala Glu Ala Phe Glu Glu Asp Thr Gly Arg Tyr
50 55 60
Ser Cys Phe Ala Ser Asn Ile Tyr Gly Thr Asp Ser Thr Ser Ala Glu
65 70 75 80
Ile Tyr Ile Glu Gly Val Ser Ser Ser Asp Ser Glu Gly Asp Pro Asn
85 90 95
Lys Glu Glu Met Asn Arg Val Arg Ala Pro Pro Ile Thr Cys Arg Asp
100 105 110
Trp Met Glu Asn Leu Ser Leu Gln Leu Leu Cys Leu Gln Arg Cys Tyr
115 120 125
Lys Ile Cys Gln Leu Leu Arg Val Ser Trp Leu Ser Leu Asn Ala Glu
130 135 140

<210> 21
<211> 381
<212> DNA
<213> homo sapiens

<400> 21
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acaggacgct attcctgctt tgcttctaac atctatggga cagattcgac ttctgctgag 240
atztatatag aaggggtttc ttcttctgac tcagaaggcg accctaacaa ggaagagatg 300
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<210> 22
<211> 126
<212> PRT
<213> homo sapiens

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<400> 22
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      20             25             30
Glu Leu Glu Asn Ser Pro Asp Ile His Ile Val Gln Ala Gly Asn Leu
      35             40             45
His Ser Leu Thr Ile Ala Glu Ala Phe Glu Glu Asp Thr Gly Arg Tyr
      50             55             60
Ser Cys Phe Ala Ser Asn Ile Tyr Gly Thr Asp Ser Thr Ser Ala Glu
      65             70             75             80
Ile Tyr Ile Glu Gly Val Ser Ser Ser Asp Ser Glu Gly Asp Pro Asn
      85             90             95
Lys Glu Glu Met Asn Arg Val Arg Ala Pro Pro Ile Thr Cys Arg Asp
      100            105            110
Trp Met Glu Asn Leu Ser Leu Gln Leu Leu Cys Leu Gln Arg
      115            120            125

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<210> 23
<211> 555
<212> DNA
<213> homo sapiens

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<400> 23
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cacatcgctc aggcaggaaa tctgcactca ctgaccattg cggaagcctt tgaagaggac 180
acaggacgct attcctgctt tgcttctaac atctatggga cagattcgac ttctgctgag 240
atztatatag aaggggtttc ttcttctgac tcagaaggcg accctaacaa ggaagagatg 300
aatcgaatcc agaagccaaa tgagggtgtc tctcctccca ctacctctgc agtcattcct 360
ccagcagtac cccaagccca gcatttggtg gcccaacctc gtgtggcaac catccagcag 420
tgtcagagcc ccaccaatta cttgcaggga ttggatggaa aacctatcat tgcagctcct 480
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<210> 24
<211> 184
<212> PRT
<213> homo sapiens

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<400> 24
Met Leu Thr Val Gln Val Lys Thr Ser Ser Ala Ile Glu Leu Pro Asp
 1             5             10             15
Ser Leu Ala Phe Leu Trp Ile Ile Pro Met Trp Tyr Cys Glu Gly Lys

```


His Ser Leu Thr Ile Ala Glu Ala Phe Glu Glu Asp Thr Gly Arg Tyr
 50 55 60
 Ser Cys Phe Ala Ser Asn Ile Tyr Gly Thr Asp Ser Thr Ser Ala Glu
 65 70 75 80
 Ile Tyr Ile Glu Gly Val Ser Ser Ser Asp Ser Glu Gly Asp Pro Asn
 85 90 95
 Lys Glu Glu Met Asn Arg Ile Gln Lys Pro Asn Glu Val Ser Ser Pro
 100 105 110
 Pro Thr Thr Ser Ala Val Ile Pro Pro Ala Val Pro Gln Ala Gln His
 115 120 125
 Leu Val Ala Gln Pro Arg Val Ala Thr Ile Gln Gln Cys Gln Ser Pro
 130 135 140
 Thr Asn Tyr Leu Gln Gly Leu Asp Gly Lys Pro Ile Ile Ala Ala Pro
 145 150 155 160
 Val Phe Thr Lys Met Leu Gln Asn Leu Ser Ala Ser Glu Gly Gln Leu
 165 170 175
 Val Val Phe Glu Cys Arg Val Lys Gly Ala Pro Ser Pro Lys Val Glu
 180 185 190
 Trp Tyr Arg Glu Gly Thr Leu Ile Glu Asp Ser Pro Asp Phe Arg Ile
 195 200 205
 Leu Gln Lys Lys Pro Arg Ser Met Ala Glu Pro Glu Glu Ile Cys Thr
 210 215 220
 Leu Val Ile Ala Glu Val Phe Ala Glu Asp Ser Gly Cys Phe Thr Cys
 225 230 235 240
 Thr Ala Ser Asn Lys Tyr Gly Thr Val Ser Ser Ile Ala Gln Leu His
 245 250 255
 Val Arg Gly Asn Glu Asp Leu Ser Asn Asn Gly Ser Leu His Ser Ala
 260 265 270
 Asn Ser Thr Thr Asn Leu Ala Ala Ile Tyr Pro Ile Ala Pro Pro Leu
 275 280 285
 Pro Pro Leu Glu Pro Lys Lys
 290 295

<210> 27

<211> 1440

<212> DNA

<213> homo sapiens

<400> 27

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cacatcgccc	aggcaggaaa	tctgcactca	ctgaccattg	cggaagcctt	tgaagaggac	180
acaggacgct	attcctgctt	tgcttctaac	atctatggga	cagattcgac	ttctgctgag	240
atcttatatag	aaggggtttc	ttcttctgac	tcagaaggcg	accctaacaa	ggaagagatg	300
aatcgaatcc	agaagccaaa	tgagggtgtca	tctcctccca	ctacctctgc	agtcattcct	360
ccagcagtac	cccaagccca	gcatttgggtg	gccaacctc	gtgtggcaac	catccagcag	420
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gtgtttacaa	agatgctaca	aaatttgtca	gcttctgagg	gtcagctggg	tgtctttgaa	540
tgcagagtaa	aaggagctcc	atctcctaag	gttgagtggg	atagagaagg	gactttaata	600
gaagattctc	cagatttttag	gattttacag	aaaaaacctc	gatccatggc	agagccagag	660
gagatttgca	ccttgggtcat	tgctgagggtg	tttgccagaag	attctgggtg	cttcacatgt	720
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gaggacctca	gcaacaacgg	gtctcttcac	tcagccaact	cyaccaccaa	cctggcagct	840
attgagccac	agccctcccc	accccaactc	gagcctccat	ctgtggaaca	accccccaaa	900
cccaaactcg	aggggggttct	ggtgaaccac	aatgagcccc	ggtccagctc	caggattggg	960
cttcgtgtgc	acttcaacct	gcctgaagat	gacaaaggaa	gtgaagcatc	ctccgaggct	1020


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ggtgtggtga ccaccagaca gaccaggccc gattctttsc aggagagggtt caacggacag 1080
gcaacaaaaa cccagagacc ttctttcccc gtgaaagagc cccctccagt tctggccaaa 1140
cccaaacttg attccactca gttacaacag cttcataacc aagtcttact ggaacaacac 1200
caattgcaaa acccacctcc ttcatctcct aaggagtttc ctttcarcat gactgttttg 1260
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cagacgttca gcttggcccg gccgaagtat ttcttccctt ccacgaacac caccgcagca 1380
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<210> 28
<211> 479
<212> PRT
<213> homo sapiens

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<220>
<221> VARIANT
<222> (1)...(479)
<223> Xaa = Any Amino Acid

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<400> 28
Met Leu Thr Val Gln Val Lys Thr Ser Ser Ala Ile Glu Leu Pro Asp
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Ser Leu Ala Phe Leu Trp Ile Ile Pro Met Trp Tyr Cys Glu Gly Lys
20        25        30
Glu Leu Glu Asn Ser Pro Asp Ile His Ile Val Gln Ala Gly Asn Leu
35        40        45
His Ser Leu Thr Ile Ala Glu Ala Phe Glu Glu Asp Thr Gly Arg Tyr
50        55        60
Ser Cys Phe Ala Ser Asn Ile Tyr Gly Thr Asp Ser Thr Ser Ala Glu
65        70        75        80
Ile Tyr Ile Glu Gly Val Ser Ser Ser Asp Ser Glu Gly Asp Pro Asn
85        90        95
Lys Glu Glu Met Asn Arg Ile Gln Lys Pro Asn Glu Val Ser Ser Pro
100       105       110
Pro Thr Thr Ser Ala Val Ile Pro Pro Ala Val Pro Gln Ala Gln His
115       120       125
Leu Val Ala Gln Pro Arg Val Ala Thr Ile Gln Gln Cys Gln Ser Pro
130       135       140
Thr Asn Tyr Leu Gln Gly Leu Asp Gly Lys Pro Ile Ile Ala Ala Pro
145       150       155       160
Val Phe Thr Lys Met Leu Gln Asn Leu Ser Ala Ser Glu Gly Gln Leu
165       170       175
Val Val Phe Glu Cys Arg Val Lys Gly Ala Pro Ser Pro Lys Val Glu
180       185       190
Trp Tyr Arg Glu Gly Thr Leu Ile Glu Asp Ser Pro Asp Phe Arg Ile
195       200       205
Leu Gln Lys Lys Pro Arg Ser Met Ala Glu Pro Glu Glu Ile Cys Thr
210       215       220
Leu Val Ile Ala Glu Val Phe Ala Glu Asp Ser Gly Cys Phe Thr Cys
225       230       235       240
Thr Ala Ser Asn Lys Tyr Gly Thr Val Ser Ser Ile Ala Gln Leu His
245       250       255
Val Arg Gly Asn Glu Asp Leu Ser Asn Asn Gly Ser Leu His Ser Ala
260       265       270
Asn Ser Thr Thr Asn Leu Ala Ala Ile Glu Pro Gln Pro Ser Pro Pro
275       280       285
His Ser Glu Pro Pro Ser Val Glu Gln Pro Pro Lys Pro Lys Leu Glu

```

290		295		300
Gly Val Leu Val Asn His Asn Glu Pro Arg Ser Ser Ser Arg Ile Gly				
305		310		320
Leu Arg Val His Phe Asn Leu Pro Glu Asp Asp Lys Gly Ser Glu Ala				
	325		330	335
Ser Ser Glu Ala Gly Val Val Thr Thr Arg Gln Thr Arg Pro Asp Ser				
	340		345	350
Xaa Gln Glu Arg Phe Asn Gly Gln Ala Thr Lys Thr Pro Glu Pro Ser				
	355		360	365
Phe Pro Val Lys Glu Pro Pro Pro Val Leu Ala Lys Pro Lys Leu Asp				
	370		375	380
Ser Thr Gln Leu Gln Gln Leu His Asn Gln Val Leu Leu Glu Gln His				
385		390		395
Gln Leu Gln Asn Pro Pro Pro Ser Ser Pro Lys Glu Phe Pro Phe Xaa				
	405		410	415
Met Thr Val Leu Asn Ser Asn Ala Pro Pro Ala Val Thr Thr Ser Xaa				
	420		425	430
Lys Gln Val Lys Ala Pro Ser Ser Gln Thr Phe Ser Leu Ala Arg Pro				
	435		440	445
Lys Tyr Phe Phe Pro Ser Thr Asn Thr Thr Ala Ala Thr Val Ala Pro				
	450		455	460
Ser Ser Ser Pro Val Phe Thr Leu Ser Ser Ile Pro Pro Gln Thr				
465		470		475